# GENDEX: The ALPHA, CIB, RCD, and RRC MODULES

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ABSTRACT

Details are presented for obtaining randomized plans for various experiment designs. Four of the ten modules in the Gendex toolkit are discussed here. They are the ALPHA module, the CIB module, the RCD module, and the RRC modules. The ALPHA module is used to obtain randomized plans for incomplete block experiment designs. The number of treatments that may be included is between 2 and 10,000. Variable block sizes and numbers of replicates are available. The CIB module may be used to obtain randomized plans for incomplete block experiment designs for any number of treatments between 2 and 10,000. Variable numbers of block sizes and replications are available. This module may also be used to obtain certain k-row by s-column experiment designs. The RCD module is used to construct randomized plans for k-row by s-column experiment designs. The RRC module is utilized to construct randomized plans for resolvable row-column (lattice rectangle) experiment designs. Each complete block has k rows and s columns. Here the number of treatments v = ks. These last two modules require that an incomplete block experiment design be constructed first as the input file and this is changed into an optimal or near optimal row-column experiment design by a process of successive iterations.

Keywords: Randomized plan, incomplete block experiment design, row-column experiment designs, resolvable row-column experiment designs, lattice rectangle design, efficiency factor, optimal design, alpha-type experiment design, Youden-type experiment design.

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## INTRODUCTION

In a previous technical report, Federer, Gross, Nguyen, and Nshinyabakobeje (2001) describe the procedure for installing the Gendex toolkit and for using the BIB module to construct randomized plans for $2 \leq v \leq 200$ treatments in incomplete blocks of sizes $2 \leq k \leq v \leq 20$ with $2 \leq r \leq 20$ replications (complete blocks). The Gendex toolkit has five modules that may be used to construct various types of experiment designs. The other four design construction modules are the ALPHA module, the CIB module, the RCD module, and the RRC module.

The ALPHA module is used to construct randomized plans for the alpha-type incomplete block experiment designs. The number of treatments v that may be accommodated with this type of design is between 4 and 10,000. Available block sizes are $r \leq k \leq 100$. The number of blocks per complete block (replicate) is $2 \leq s \leq 100$. The number of replications available is $2 \leq r \leq 10$. A number of tries and a number of iterations for each try are used until an optimal or near optimal design is obtained.

The CIB module may be used to construct randomized plans for $2 \leq v \leq 10{,}000$ treatments in incomplete blocks of sizes $2 \leq k < v \leq 20$ with $2 \leq r \leq 20$ replications of each treatment. Certain k-row by s-column experiment designs may also be constructed with this module. Starting with an initial block and using cyclical permutations of that block an incomplete block experiment design is constructed. The program tries various initial blocks and various numbers of iterations until optimality or near optimality is achieved.

The RCD module may be utilized to construct randomized plans for a k-row by b-column experiment design. Here the relation $vr = kb$ must hold. An optimal or near optimal incomplete block design is constructed using either the ALPHA, the BIB, or the CIB module. The incomplete blocks are completely randomized and therefore are not in complete blocks. This design is the starting point for obtaining an optimal or near optimal row-column experiment design.

Resolvable row-column (RRC) or lattice rectangle experiment designs have k rows and s columns in each complete block (replication). Here the number of treatments $v = ks$. The starting point for constructing these designs is to obtain an optimal or near optimal incomplete block experiment design using either the ALPHA or the BIB module. The incomplete block experiment design is 1-resolvable, i.e., it has complete blocks with each of the v treatments occurring once in each of the r complete blocks. This design is the input design for the RRC module. The treatments in the incomplete blocks (rows) are rearranged so that an optimal or near optimal incomplete block design is formed for columns and treatments.

These modules need to be placed in a folder. Set up a New Folder by going to START, then to PROGRAMS, and then to WINDOWS EXPLORER. Under FILE, click on NEW and then on FOLDER. Right click on the New Folder and select Rename. We rename the New Folder as Gendex. All modules are placed in this folder as explained in Federer, Gross, Nguyen, and Nishinyabakobeje (2001). This is accomplished by going to the place where e-mail attachments reside. This is C:\PROGRAM FILES\BEAR ACCESS\WINBA\EUDORA\ATTACH in our case. Highlight the attachment and select

COPY. PASTE the file in the Gendex folder. Then unzip the file if necessary as explained in the previous cited reference.

## ALPHA MODULE

The ALPHA module may be used to construct alpha-type incomplete block experiment designs (Patterson and Williams, 1976; Patterson, Williams, and Patterson. 1985). These designs are all 1-resolvable experiment designs. The construction is obtained via the selection (automatic) of an alpha r × k array. The symbol r is used for the number of replicates, $2 \leq r \leq 10$. The symbol k is the incomplete block size, $r \leq k \leq 100$. The symbol s is used to designate the number of incomplete blocks per replicate, $2 \leq s \leq 100$. The letter v designates the number of treatments, $4 \leq v = ks \leq 10{,}000$. Thus, randomized plans for incomplete block experiment designs can be constructed for large numbers of treatments as frequently used by plant breeders, for example.

The following steps are used to obtain an alpha-type incomplete block experiment design:

1. Go to START/PROGRAMS/MS_DOS PROMPT.
2. Type the command CD\GENDEX, and hit return key.
3. Type the command java -cp C:\Gendex Alpha, and hit return key. Note that the word Alpha must be typed in this exact form.
4. A number prompts are given:
   Choose the number of replicates (r):
   Choose the block size (k):
   Choose the number of blocks per replicate (s):
   Do you want to print blocks as columns? YES or NO. If NO is clicked blocks are rows.
   Enter a random seed:
   Enter the number of tries:

One may simply click OK for the last two prompts or enter some number. For the following example, r = 3, k = 4, s = 6, and a random seed = 1123 was selected. Using the same random seed produces the same randomized plan. The number of treatments v = ks = 4(6) = 24. The output obtained for this design is given below:

ALPHA 2.0: Construct Alpha designs of size (r,k,s)
(C) 2001 Design Computing (URL: http://designcomputing.hypermart.net/gendex)

Note: Alpha design for v=24, r=3, k=4, s=6.

| | |
|---|---|
| try # | 1 |
| seed | 1123 |
| # of iterations | 4 |
| E | 0.7265 |
| E/U | 0.993 |
| concurrences | 0(168) 1(108) |

| | |
|---|---|
| try # | 3 |
| seed | -421466239 |

| | |
|---|---|
| # of iterations | 3 |
| E | 0.7265 |
| E/U | 0.993 |
| concurrences | 0(168) 1(108) |

Alpha array (r x k):

| | | | |
|---|---|---|---|
| 0 | 0 | 0 | 0 |
| 5 | 3 | 2 | 0 |
| 2 | 3 | 1 | 4 |

Plan (Blocks are rows):

| | | | |
|---|---|---|---|
| 16 | 4 | 22 | 10 |
| 14 | 20 | 8 | 2 |
| 6 | 18 | 0 | 12 |
| 23 | 17 | 5 | 11 |
| 15 | 3 | 21 | 9 |
| 13 | 1 | 19 | 7 |

| | | | |
|---|---|---|---|
| 20 | 16 | 1 | 11 |
| 6 | 17 | 21 | 2 |
| 19 | 0 | 10 | 15 |
| 13 | 4 | 23 | 8 |
| 18 | 5 | 9 | 14 |
| 22 | 12 | 3 | 7 |

| | | | |
|---|---|---|---|
| 11 | 15 | 18 | 4 |
| 19 | 16 | 5 | 6 |
| 7 | 20 | 0 | 17 |
| 21 | 12 | 1 | 8 |
| 23 | 14 | 3 | 10 |
| 13 | 2 | 22 | 9 |

Note: ALPHA used 0.28 seconds.
Note: this software is licensed to AV Biometrics.

Click OK at the bottom of the screen and a note will appear saying that this output has been saved as ALPHA.HTM in the Gendex folder. The ALPHA.HTM file was highlighted. Using the SELECT ALL, COPY, and PASTE commands, the output was pasted in this document. Pasting the output in any word processing package allows it to be edited. The E/U ratio of 0.993 is close to one and hence this design is near optimal if not the best that can be obtained.

The restriction $r \leq k$ can be by-passed. For example, suppose that an experimenter desires $r = 6$ and $k = 4$, say. One design for $r = k = 4$ can be obtained. Then, another design for $r = 2$ and $k = 4$ can be constructed. Putting these two together, one has the desired replication. This design may not be optimal but will have a high E/U ratio. This is akin to using two sets of a triple lattice experiment design to obtain $r = 6$ replicates from a design with three arrangements of treatments in the incomplete blocks.

For a second example, let $r = 2$, $k = 10$, and $s = 30$. Then v will be 300.

ALPHA 2.0: Construct Alpha designs of size (r,k,s)

Note: Alpha design for v=300, r=2, k=10, s=30.

| | |
|---|---|
| try # | 1 |
| seed | 1003526792410 |
| # of iterations | 5 |
| E | 0.8176 |
| E/U | 0.9998 |
| concurrences | 0(42150) 1(2700) |

Alpha array (r x k):

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 14 | 27 | 7 | 0 | 9 | 12 | 19 | 6 | 23 | 8 |

Plan (Blocks are rows):

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 72 | 282 | 42 | 132 | 162 | 12 | 222 | 102 | 192 | 252 |
| 84 | 24 | 114 | 264 | 294 | 204 | 144 | 174 | 234 | 54 |
| 124 | 244 | 34 | 64 | 214 | 4 | 94 | 274 | 154 | 184 |
| 65 | 155 | 185 | 245 | 275 | 215 | 95 | 125 | 35 | 5 |
| 110 | 230 | 170 | 260 | 290 | 50 | 80 | 20 | 140 | 200 |
| 285 | 75 | 195 | 15 | 45 | 105 | 225 | 255 | 165 | 135 |
| 143 | 23 | 203 | 233 | 263 | 83 | 53 | 293 | 113 | 173 |
| 186 | 216 | 6 | 276 | 66 | 126 | 246 | 96 | 36 | 156 |
| 106 | 256 | 196 | 136 | 226 | 286 | 46 | 76 | 166 | 16 |
| 148 | 208 | 118 | 58 | 238 | 268 | 298 | 178 | 88 | 28 |
| 115 | 295 | 55 | 205 | 25 | 265 | 175 | 85 | 235 | 145 |
| 153 | 183 | 33 | 63 | 3 | 213 | 123 | 243 | 273 | 93 |
| 190 | 160 | 100 | 220 | 280 | 70 | 250 | 10 | 130 | 40 |
| 127 | 277 | 7 | 37 | 97 | 217 | 67 | 247 | 187 | 157 |
| 71 | 131 | 191 | 251 | 101 | 221 | 41 | 281 | 161 | 11 |
| 253 | 73 | 103 | 13 | 283 | 193 | 133 | 43 | 163 | 223 |
| 177 | 117 | 297 | 207 | 57 | 147 | 267 | 87 | 237 | 27 |
| 146 | 206 | 176 | 86 | 296 | 26 | 236 | 266 | 116 | 56 |
| 169 | 229 | 289 | 199 | 259 | 49 | 19 | 79 | 109 | 139 |
| 62 | 152 | 122 | 2 | 182 | 92 | 242 | 272 | 212 | 32 |
| 69 | 219 | 159 | 39 | 189 | 279 | 99 | 9 | 129 | 249 |
| 209 | 179 | 149 | 299 | 269 | 89 | 59 | 119 | 239 | 29 |
| 164 | 134 | 104 | 224 | 284 | 254 | 44 | 14 | 194 | 74 |
| 150 | 180 | 240 | 60 | 90 | 210 | 120 | 270 | 0 | 30 |
| 262 | 292 | 232 | 142 | 82 | 202 | 22 | 172 | 52 | 112 |
| 218 | 248 | 98 | 158 | 38 | 278 | 68 | 188 | 8 | 128 |
| 108 | 288 | 198 | 168 | 78 | 48 | 18 | 138 | 228 | 258 |
| 47 | 197 | 167 | 257 | 227 | 107 | 137 | 287 | 17 | 77 |
| 291 | 171 | 51 | 81 | 201 | 261 | 21 | 111 | 141 | 231 |
| 91 | 121 | 181 | 61 | 271 | 31 | 211 | 151 | 1 | 241 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 49 | 154 | 238 | 255 | 89 | 191 | 121 | 112 | 270 | 6 |
| 157 | 273 | 211 | 258 | 62 | 124 | 52 | 194 | 9 | 115 |
| 240 | 169 | 223 | 285 | 97 | 206 | 74 | 136 | 34 | 21 |
| 116 | 125 | 259 | 274 | 10 | 53 | 63 | 158 | 212 | 195 |
| 248 | 105 | 184 | 29 | 42 | 293 | 231 | 144 | 177 | 82 |
| 225 | 76 | 99 | 287 | 242 | 36 | 171 | 138 | 208 | 23 |
| 181 | 174 | 228 | 26 | 79 | 290 | 141 | 39 | 102 | 245 |
| 193 | 61 | 8 | 210 | 114 | 51 | 123 | 257 | 272 | 156 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 172 | 139 | 288 | 243 | 100 | 226 | 24 | 37 | 77 | 209 |
| 57 | 90 | 14 | 129 | 278 | 67 | 263 | 162 | 216 | 199 |
| 80 | 229 | 103 | 40 | 246 | 142 | 27 | 291 | 182 | 175 |
| 251 | 147 | 2 | 234 | 187 | 85 | 150 | 45 | 296 | 108 |
| 201 | 69 | 218 | 16 | 59 | 131 | 265 | 280 | 164 | 92 |
| 64 | 126 | 196 | 159 | 11 | 213 | 117 | 275 | 54 | 260 |
| 165 | 70 | 17 | 266 | 219 | 202 | 281 | 93 | 30 | 132 |
| 268 | 283 | 167 | 19 | 32 | 95 | 221 | 134 | 204 | 72 |
| 215 | 13 | 198 | 161 | 66 | 277 | 56 | 262 | 119 | 128 |
| 68 | 91 | 279 | 130 | 217 | 58 | 15 | 264 | 200 | 163 |
| 35 | 75 | 170 | 286 | 98 | 224 | 137 | 241 | 207 | 22 |
| 113 | 271 | 192 | 239 | 60 | 50 | 256 | 155 | 7 | 122 |
| 41 | 104 | 247 | 292 | 183 | 81 | 230 | 28 | 143 | 176 |
| 110 | 152 | 298 | 236 | 253 | 4 | 87 | 149 | 189 | 47 |
| 179 | 146 | 233 | 186 | 107 | 44 | 250 | 295 | 84 | 1 |
| 168 | 73 | 222 | 135 | 20 | 269 | 33 | 96 | 284 | 205 |
| 111 | 153 | 48 | 88 | 237 | 190 | 299 | 254 | 5 | 120 |
| 178 | 106 | 145 | 294 | 43 | 249 | 232 | 0 | 83 | 185 |
| 197 | 127 | 214 | 65 | 276 | 12 | 118 | 261 | 55 | 160 |
| 31 | 282 | 166 | 203 | 220 | 18 | 71 | 267 | 94 | 133 |
| 244 | 289 | 25 | 180 | 227 | 38 | 78 | 101 | 173 | 140 |
| 188 | 109 | 151 | 235 | 3 | 252 | 46 | 86 | 297 | 148 |

Note: ALPHA used 0.33 seconds.
Note: this software is licensed to AV Biometrics.

The E/U ratio of 0.9998 is very close to one. This design required only 0.33 seconds of computer time to obtain the randomized plan for $v = 300$ treatments in incomplete blocks of size $k = 10$ in $r = 2$ replicates.

## CIB MODULE

This module produces randomized plans for $2 \leq v \leq 10{,}000$ treatments in incomplete blocks of size $2 \leq k < v \leq 20$ in $2 \leq r \leq 20$ replications. No complete block options with the CIB module are possible, i.e., no resolvable plan is possible. The designs are constructed via cyclical permutations of an initial block. The program tries various initial blocks until one achieves optimality or near optimality. The incomplete blocks are randomly arranged and the treatments within an incomplete block are also randomly arranged. For certain values of k and r, a row-column experiment design of the Youden-type is an option. A Youden-type experiment design is one where all v treatments occur in each row and the treatments and columns form a balanced or nearly balanced incomplete block experiment design. Thus this module may be used to construct randomized incomplete block experiment designs or row-column experiment designs. If k is a factor of v, r may take on the values 2, 3, 4, 5, .... If k/c is a factor of v, r may take on the values 2c, 3c, 4c, 5c, .... If k is not a factor of v, r may take on the values k, 2k, 3k, 4k, 5k,.... When r = k, 2k, 3k, 4k, 5k, ..., a Youden-type design may be constructed if desired. When k is not a factor of r, e.g., v = 12, r = 5, and k = 4, there will not be a prompt asking if a Youden-type design is desired. Within these limitations on the values of r and k, any incomplete block or row-column Youden-type experiment design may be constructed.

The Cib module is activated using the following steps together with the selections made for an example using v = 12 treatments, k = 4 as the block size, and r = 4 replications:

1. Go to START/PROGRAMS/MS_DOS PROMPT.
2. Use CD\ Gendex to change directory to the C:\Gendex > directory where the Gendex folder resides..
3. Use the command: C:\ >java -cp C:\Gendex Cib and hit return to start the design construction. Not that The form Cib must be used as the program is case sensitive.
4. Answer the following prompts
   Choose the number of treatments? Clicked on 12 for the following example. Then OK.
   Choose the block size: Clicked on ; then on OK.
   Choose the number of replicates: Clicked on 4; then on OK.
   Do you want to construct a Youden-type design: Clicked on YES.
   Do you want to print blocks as columns: Clicked on YES.
   Enter a random seed: Was left blank. Clicked on Cancel.
   Enter the number of tries: Was left blank. Clicked on Cancel.

The following output was obtained:

CIB 2.2: Construct cyclic incomplete block designs of size (v,k,r)
(C) 2001 Design Computing (URL: http://designcomputing.hypermart.net/gendex)

Note: Cyclic incomplete block design for v=12, k=4, r=4, b=12.

| | |
|---|---|
| try # | 1 |
| seed | 1002047204770 |
| # of iterations | 1 |
| E | 0.8133803 |
| E/U | 1 |
| concurrences | 1(10) 2(1) |

Initial block(s) and the # of blocks/replications generated by each initial block:

0 6 7 10 (4)

Plan (Blocks are columns):

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | 8 | 7 | 11 | 5 | 3 | 1 | 4 | 0 | 6 | 9 | 10 |
| 8 | 2 | 1 | 5 | 11 | 9 | 7 | 10 | 6 | 0 | 3 | 4 |
| 9 | 3 | 2 | 6 | 0 | 10 | 8 | 11 | 7 | 1 | 4 | 5 |
| 0 | 6 | 5 | 9 | 3 | 1 | 11 | 2 | 10 | 4 | 7 | 8 |

Note: CIB used 0.06 seconds.
Note: this software is licensed to AV Biometrics.

This 4-row by 12-column Youden-type experiment design is optimal since E/U = 1. Note that all 12 treatments occur once in each row of the design. Therefore, rows and treatments are in an orthogonal arrangement. The concurrence display is different from

that obtained with the BIB module. Here 1(10) means that any treatment occurs with 10 other treatments in one of the 12 columns (incomplete blocks) and 2(1) means that a treatment occurs two times with one other treatment in the 12 columns. The CIB module uses cyclical permutations to construct a design, generating the other blocks from the initial block. This design was obtained at the first try and first iteration. Only 0.06 seconds of computer time was used. The prompt Do you want a Youden-type design only occurs for cetain values of k and r. For example it does not occur for v = 9, r = 6, and k = 2.

As a second example, let v = 225 treatments, k = 15 the block size, and r = 3 replications. Following the steps outlined above, the output obtained was:

CIB 2.2: Construct cyclic incomplete block designs of size (v,k,r)
(C) 2001 Design Computing (URL: http://designcomputing.hypermart.net/gendex)

Note: Cyclic incomplete block design for v=225, k=15, r=3, b=45.

| | |
|---|---|
| try # | 1 |
| seed | 1002051861350 |
| # of iterations | 5 |
| E | 0.91364473 |
| E/U | 0.9993 |
| concurrences | 0(14) 1(30) |

| | |
|---|---|
| try # | 2 |
| seed | -735098249 |
| # of iterations | 6 |
| E | 0.91369826 |
| E/U | 0.9994 |
| concurrences | 0(14) 1(30) |

| | |
|---|---|
| try # | 3 |
| seed | 818049685 |
| # of iterations | 5 |
| E | 0.9139779 |
| E/U | 0.9997 |
| concurrences | 0(14) 1(30) |

| | |
|---|---|
| try # | 4 |
| seed | 986248891 |
| # of iterations | 5 |
| E | 0.91400677 |
| E/U | 0.9997 |
| concurrences | 0(14) 1(30) |

Initial block(s) and the # of blocks/replications generated by each initial block:

0 6 25 (3)
0 16 28 (3)
0 7 37 (3)
0 1 3 (3)
0 21 11 (3)

Plan (Blocks are rows):

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 137 | 95 | 210 | 177 | 197 | 34 | 198 | 126 | 52 | 49 | 78 | 163 | 14 | 101 | 23 |
| 97 | 199 | 135 | 192 | 20 | 42 | 137 | 127 | 53 | 186 | 46 | 77 | 41 | 179 | 116 |
| 79 | 90 | 135 | 176 | 40 | 33 | 200 | 120 | 87 | 92 | 5 | 51 | 196 | 177 | 191 |
| 85 | 182 | 133 | 107 | 38 | 165 | 176 | 190 | 55 | 111 | 180 | 63 | 137 | 13 | 44 |
| 112 | 29 | 165 | 183 | 10 | 202 | 216 | 135 | 67 | 18 | 48 | 134 | 130 | 162 | 80 |
| 19 | 194 | 93 | 98 | 176 | 31 | 217 | 121 | 69 | 12 | 57 | 160 | 209 | 81 | 162 |
| 168 | 204 | 160 | 214 | 189 | 131 | 1 | 102 | 165 | 54 | 117 | 23 | 27 | 70 | 71 |
| 20 | 36 | 168 | 126 | 149 | 132 | 203 | 224 | 73 | 129 | 76 | 181 | 162 | 16 | 56 |
| 40 | 218 | 166 | 206 | 149 | 160 | 4 | 125 | 222 | 88 | 97 | 17 | 72 | 60 | 95 |
| 50 | 219 | 120 | 166 | 44 | 127 | 123 | 184 | 195 | 168 | 153 | 59 | 22 | 15 | 74 |
| 86 | 223 | 8 | 149 | 210 | 188 | 153 | 151 | 90 | 68 | 6 | 111 | 47 | 29 | 115 |
| 83 | 28 | 11 | 166 | 150 | 198 | 134 | 151 | 12 | 193 | 84 | 114 | 107 | 65 | 186 |
| 187 | 89 | 1 | 112 | 153 | 191 | 24 | 121 | 3 | 164 | 108 | 192 | 52 | 150 | 62 |
| 180 | 164 | 64 | 147 | 77 | 205 | 151 | 93 | 61 | 16 | 102 | 200 | 37 | 7 | 100 |
| 216 | 75 | 150 | 104 | 201 | 129 | 143 | 26 | 35 | 190 | 4 | 45 | 117 | 147 | 87 |
| 91 | 32 | 66 | 202 | 132 | 220 | 58 | 164 | 143 | 85 | 217 | 21 | 141 | 15 | 95 |
| 212 | 8 | 214 | 141 | 127 | 124 | 125 | 25 | 9 | 175 | 48 | 82 | 78 | 147 | 209 |
| 224 | 175 | 49 | 81 | 90 | 113 | 28 | 189 | 30 | 53 | 123 | 143 | 43 | 155 | 185 |
| 51 | 107 | 207 | 118 | 70 | 24 | 157 | 203 | 115 | 218 | 0 | 46 | 39 | 141 | 155 |
| 114 | 175 | 94 | 7 | 157 | 56 | 206 | 219 | 215 | 14 | 2 | 171 | 112 | 79 | 55 |
| 99 | 80 | 34 | 155 | 108 | 63 | 41 | 184 | 188 | 171 | 26 | 213 | 93 | 169 | 72 |
| 223 | 157 | 57 | 122 | 67 | 42 | 32 | 169 | 174 | 5 | 198 | 117 | 211 | 100 | 59 |
| 33 | 69 | 171 | 193 | 132 | 68 | 54 | 140 | 174 | 192 | 104 | 38 | 208 | 9 | 96 |
| 119 | 187 | 145 | 200 | 169 | 125 | 65 | 71 | 140 | 43 | 91 | 221 | 10 | 13 | 76 |
| 145 | 146 | 89 | 0 | 123 | 73 | 174 | 18 | 190 | 205 | 60 | 197 | 109 | 31 | 124 |
| 19 | 23 | 110 | 201 | 140 | 74 | 148 | 199 | 2 | 202 | 64 | 88 | 146 | 115 | 113 |
| 128 | 209 | 145 | 139 | 196 | 27 | 34 | 50 | 75 | 118 | 20 | 114 | 148 | 220 | 47 |
| 105 | 108 | 146 | 42 | 139 | 159 | 40 | 94 | 66 | 86 | 212 | 189 | 36 | 182 | 84 |
| 183 | 185 | 17 | 148 | 62 | 99 | 44 | 106 | 83 | 159 | 33 | 152 | 78 | 203 | 100 |
| 52 | 138 | 139 | 61 | 29 | 22 | 206 | 194 | 104 | 53 | 122 | 103 | 207 | 13 | 152 |
| 170 | 159 | 96 | 12 | 18 | 215 | 184 | 101 | 204 | 77 | 51 | 45 | 6 | 138 | 91 |
| 152 | 19 | 223 | 119 | 181 | 178 | 213 | 124 | 1 | 58 | 87 | 116 | 170 | 11 | 55 |
| 85 | 138 | 3 | 113 | 92 | 109 | 211 | 156 | 82 | 193 | 16 | 27 | 222 | 178 | 80 |
| 208 | 57 | 4 | 49 | 170 | 173 | 133 | 156 | 36 | 187 | 37 | 195 | 110 | 48 | 118 |
| 46 | 35 | 221 | 94 | 128 | 15 | 167 | 178 | 173 | 17 | 205 | 81 | 54 | 130 | 210 |
| 161 | 167 | 79 | 105 | 22 | 186 | 156 | 8 | 21 | 99 | 70 | 76 | 197 | 201 | 98 |
| 25 | 131 | 106 | 60 | 220 | 56 | 122 | 158 | 173 | 199 | 6 | 28 | 63 | 191 | 161 |
| 167 | 96 | 72 | 103 | 126 | 212 | 74 | 180 | 67 | 11 | 154 | 196 | 158 | 24 | 30 |
| 69 | 216 | 154 | 3 | 47 | 172 | 59 | 7 | 185 | 161 | 101 | 119 | 39 | 182 | 97 |
| 71 | 207 | 68 | 14 | 84 | 26 | 37 | 109 | 183 | 217 | 120 | 116 | 172 | 144 | 158 |
| 62 | 215 | 32 | 154 | 41 | 136 | 111 | 194 | 110 | 144 | 35 | 73 | 214 | 65 | 92 |
| 204 | 61 | 128 | 89 | 142 | 5 | 172 | 224 | 133 | 134 | 21 | 136 | 88 | 9 | 213 |
| 144 | 50 | 121 | 64 | 218 | 130 | 211 | 105 | 163 | 45 | 142 | 38 | 25 | 181 | 43 |
| 30 | 86 | 10 | 179 | 163 | 58 | 222 | 0 | 98 | 219 | 208 | 106 | 102 | 75 | 136 |
| 131 | 83 | 103 | 31 | 179 | 142 | 129 | 221 | 188 | 177 | 39 | 2 | 195 | 66 | 82 |

Note: CIB used 0.5 seconds.
Note: this software is licensed to AV Biometrics.

This incomplete block experiment design required only 0.5 seconds of computer time whereas many hours would have been required to construct a similar plan manually. The design is nearly optimal as indicated by E/U = 0.9997 and may be the best that can be obtained. Only four tries, each starting with a different initial block, were needed and there were few iterations per try. Note that if the experiment was conducted as the above

plan, it could be considered as a 45-row (incomplete block) by 15-column experiment design. Another attempt for this v, k, and r required 43 tries and 6.15 seconds of computer time. The same E/U ratio of 0.9997 was obtained.

## RCD MODULE

This module may be used to construct a randomized plan for a k-row by b-column experiment design. An input file from a module that can construct a randomized plan for an incomplete block design is required. The ALPHA, BIB, and CIB modules are used to construct incomplete block experiment design plans. We use the BIB module to illustrate the construction of row-column experiment designs. The incomplete block experiment design should not be blocked, i.e., answer NO to the one- or two-resolvable options. To construct the incomplete block design, go to START/PROGRAMS/MS_DOS PROMPT and enter the DOS directory. Here change directory from C:\WINDOWS> to C:\Gendex> with CD\, the change directory command, assuming that a Gendex folder has been set up on the C:\ drive. Then type BIB or java -cp c:\gendex Bib in C:\Gendex>, and hit return key. Follow the menu prompts to obtain the incomplete block design for v treatments in incomplete blocks of size k and with r replicates on each treatment. When the incomplete block design appears on the screen, click OK at the bottom of the screen. A note will appear describing the incomplete block experiment design that was constructed and stating "Note: BIB.HTM has been created." This file will reside in the C:\Gendex directory.

The next step is to go to START/PROGRAMS/WINDOWS EXPLORER, click On C:\, then on Gendex, and then on BIB.HTM. OPEN BIB.HTM, click on SELECT ALL and then on COPY. Next go to START/PROGRAMS/MS_DOS PROMPT to select the DOS directory. Type the command

C:\WINDOWS>CD\GENDEX

to change the directory. Then type

C:\Gendex> notepad abc.txt

to create an input file named abc.txt, for the RCD module. At the prompt to create a new file, answer YES. Then an empty file will appear. Select PASTE from EDIT on NOTEPAD to paste BIB.HTM in notepad. Edit the file by removing all material except the randomized plan. All blank lines should be removed. SAVE the edited plan. Then type the command

C:\Gendex> RCD

The plan for the row-column design will be displayed on the screen. Click OK at the bottom of the screen and a screen will appear giving the details of the plan constructed and a note saying "Note: RCD.HTM has been created." There will be an indication, C:\Gendex>, that another incomplete block experiment design may now be constructed.

To obtain a printout of RCD.HTM, go to WINDOWS EXPLORER, click on C:\, then on Gendex, and then on RCD.HTM. OPEN this file and obtain a printout using FILE/PRINT. This file will need to be copied and pasted in WORD, NOTEPAD, or some other word processing package in order to be edited.

We shall illustrate the use of this module with an example. Let v = 7 treatments, k = 4 the block size, and r = 4 replications.

1. Open DOS by using the command START/PROGRAMS/MS_DOS PROMPT, change directory to C:\Gendex> and type the command: C:\Gendex>java -cp C:\gendex Bib or simply C:\Gendex>BIB.
2. Select v = 7 treatments at the first prompt, k = 4 as the block size at the second prompt, and r = 4 replications at the third prompt. Click NO twice when asked for a 1-resolvable or a 2-resolvable design. It is optional whether or not the number of tries and a random seed are entered. One may simply put in nothing, by clicking on Cancel, and continue the process until the plan appears on the screen.
3. Click OK at bottom of screen and a screen will appear detailing the properties of the incomplete block design just created. A note saying "BIB.HTM has been created" will appear.
4. Go to WINDOWS EXPLORER, highlight C:\ and then Gendex. Click on BIB.HTM and OPEN this file.
5. Then, SELECT ALL and COPY.
6. Return to the DOS directory.
7. If necessary, change the directory from C:\WINDOWS> to C:\Gendex> using the CD\Gendex command.
8. Use the command C:\Gendex> Notepad abc.txt, where abc.txt is to be the input file for the RCD module. Answer YES to create a new file.
9. Under EDIT, select PASTE. Then edit out all material, including blank lines, until only the randomized plan remains. Then from FILE select SAVE.
10. Then use the command C:\Gendex> RCD.
11. Select abc.txt from MENU and OPEN file.
12. When the RCD appears, click on OK at bottom of screen to save file as RCD.HTM.

The following material for v = 7 treatments, r = 4 replications, k = 4 rows, and b = 7 columns, appeared on the screen:

RCD 2.2: Construct a non-resolvable row-column design of size (r,k,b)
(C) 2001 Design Computing (URL: http://designcomputing.hypermart.net)

Note: Non-resolvable row-column design for v=7, r=4, k=4 and b=7.

| | |
|---|---|
| try # | 2 |
| seed | 1795084762 |
| # of iterations | 6 |
| f | 1181.2500 |
| E(column) | 0.8750 |
| E(row) | 1 |
| E | 0.8750 |

E/U 1.0000

| | | | | | | |
|---|---|---|---|---|---|---|
| 2 | 4 | 1 | 5 | 3 | 0 | 6 |
| 3 | 2 | 6 | 0 | 1 | 4 | 5 |
| 6 | 0 | 2 | 1 | 5 | 3 | 4 |
| 0 | 5 | 4 | 6 | 2 | 1 | 3 |

Note: RCD used 0.06 seconds.
Note: this software is licensed to AV Biometrics (Australia).

This 4-row by 7-column experiment design was obtained at the second try and 6$^{th}$ iteration. Since this is a Youden-type experiment design, a balanced incomplete experiment design of treatments in columns was obtained, and hence this is the best design that can be obtained as indicated by E/U = 1. U is the upper limit on the efficiency that can be obtained and this upper limit was reached. The E(row), efficiency factor in rows, is one because rows are orthogonal to treatments. The E = 0.8750 is the efficiency factor of the design for columns and treatments and is the product of the E(row) and E(column) efficiencies. Treatments and columns form a balanced incomplete block experiment design with every treatment occurring two times with every other treatment in the seven columns (incomplete blocks).

For a second example, suppose that an experimenter has v = 25 treatments that are to be replicated r = 4 times. It is desired to place these vr =100 experimental units in a 10 × 10 square. To do this, an incomplete experiment design for v = 25 treatments in block sizes of k = 10 with r = 4 replications is created using the BIB module. The edited randomized plan was saved as abc.txt. Then following the above steps, the output obtained was:

RCD 2.2: Construct a non-resolvable row-column design of size (r,k,b)
(C) 2001 Design Computing (URL: http://designcomputing.hypermart.net/gendex)

Note: Non-resolvable row-column design for v=25, r=4, k=10 and b=10.

| | |
|---|---|
| try # | 1 |
| seed | 1002124849760 |
| # of iterations | 30 |
| f | 2878 |
| concurrences | 1(4) 2(69) 3(158) 4(61) 5(8) |
| E(column) | 0.9295 |
| E(row) | 0.9293 |
| E | 0.8642 |
| E/U | 0.9954 |

| | |
|---|---|
| try # | 2 |
| seed | -1812447041 |
| # of iterations | 28 |
| f | 2874 |
| concurrences | 1(6) 2(64) 3(159) 4(66) 5(5) |
| E(column) | 0.9295 |
| E(row) | 0.9288 |
| E | 0.8646 |
| E/U | 0.9958 |

| | |
|---|---|
| try # | 4 |
| seed | -574111810 |
| # of iterations | 38 |
| f | 2868 |
| concurrences | 1(6) 2(63) 3(159) 4(69) 5(3) |
| E(column) | 0.9295 |
| E(row) | 0.9293 |
| E | 0.8648 |
| E/U | 0.9960 |

| | |
|---|---|
| try # | 10 |
| seed | 24500696 |
| # of iterations | 31 |
| f | 2868 |
| concurrences | 1(7) 2(60) 3(162) 4(68) 5(3) |
| E(column) | 0.9295 |
| E(row) | 0.9290 |
| E | 0.8649 |
| E/U | 0.9962 |

| | |
|---|---|
| try # | 18 |
| seed | -216112495 |
| # of iterations | 37 |
| f | 2868 |
| concurrences | 1(3) 2(72) 3(150) 4(72) 5(3) |
| E(column) | 0.9295 |
| E(row) | 0.9287 |
| E | 0.8649 |
| E/U | 0.9962 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 24 | 18 | 9 | 20 | 6 | 2 | 4 | 17 | 15 | 19 |
| 6 | 4 | 3 | 19 | 23 | 11 | 16 | 21 | 22 | 14 |
| 21 | 15 | 23 | 7 | 12 | 20 | 3 | 5 | 19 | 13 |
| 10 | 21 | 15 | 14 | 18 | 19 | 24 | 0 | 5 | 8 |
| 7 | 2 | 16 | 23 | 8 | 3 | 1 | 24 | 10 | 17 |
| 1 | 12 | 21 | 0 | 7 | 8 | 15 | 11 | 17 | 9 |
| 4 | 8 | 20 | 16 | 10 | 5 | 11 | 13 | 6 | 24 |
| 22 | 7 | 2 | 18 | 13 | 6 | 0 | 9 | 16 | 3 |
| 9 | 5 | 10 | 4 | 14 | 0 | 12 | 23 | 1 | 22 |
| 20 | 22 | 14 | 17 | 11 | 1 | 18 | 2 | 13 | 12 |

Note: RCD used 0.55 seconds.
Note: this software is licensed to AV Biometrics.

Such a design as the above will not appear in any catalogue, and if one tries to construct the design manually, it will be found to be a difficult task and the E/U ratio will be usually be unknown. The plan constructed here has an E/U ratio of 0.9962, which is very close to one. In this case E/U =1 may be impossible. Hence, this is probably the most optimal plan than can be found. Note that only 0.55 seconds of computer time was required to construct the 10-row by 10-column design. The design was constructed at the $18^{th}$ try and the $37^{th}$ iteration of that try.

RRC MODULE

This module may be used to construct randomized plans for a RRC or resolvable k-row by s-column experiment design (also called a lattice rectangle experiment design) for v = ks treatments. An input file is created from a module that can construct an incomplete block experiment design such as the BIB module described in Federer *et al.* (2001). To demonstrate the use of this module to construct RRC designs, an incomplete block experiment design for v treatments in incomplete blocks of size k and with r replications of the treatments is required. If the Gendex and BIB icons are on the DESKTOP, simply click on these icons and follow the instructions to obtain the desired incomplete block design. Click OK at bottom of screen and obtain the following message "Note: BIB.HTM has been created." This file will appear in the C:\.> or the C:\Gendex> directory, depending on which directory was used to create the incomplete block experiment design.

If one is using DOS instead of icons on the DESKTOP, go to START, then PROGRAMS, and then MS_DOS PROMPT. Go to the Gendex directory with the command

C:\WINDOWS>CD\GENDEX, return

Type in

C:\Gendex>BIB, return

Follow the steps required to obtain the input file BIB.HTM. Click OK at the bottom of the screen.

The next step is to go to WINDOWS EXPLORER by selecting START, then PROGRAMS, and then WINDOWS EXPLORER. Highlight C:\ and then highlight Gendex. OPEN the BIB.HTM file which should be the one created in the previous steps. Under EDIT, click on SELECT ALL and then click on COPY. Return to MS_DOS PROMPT. In order to make a text file in which to place the input file BIB.HTM, type the command

C:\Gendex>notepad abc.txt, return

where the input text file is named abc.txt. PASTE the BIB.HTM output into the notepad file. The next step is to edit out all material except the randomized plan of the incomplete block design. Remove all blank lines including the blank line between complete blocks. After editing, select SAVE. In DOS, type the command

C:\Gendex>RRC, return

A menu will appear; select the abc.txt. Then select OPEN and answer YES to the query about r replications, k-rows, and s-columns if these are the desired numbers. Then click on OK, OK, etc. and the randomized form of the RRC or lattice rectangle experiment

design will appear on the screen. Select OK at the bottom of the screen and a note will appear that RRC.HTM has been created.

If a printout of the contents of RRC.HTM is desired, return to WINDOWS EXPLORER and highlight C:\ and then Gendex. Then open RRC.HTM and select PRINT from FILE to print out the contents of the file RRC.HTM. If only the randomized design is desired, it will be necessary to COPY and PASTE the RRC.HTM file into WORD, NOTEPAD, or other package in order to edit the file before printing.

An example for v = 12 treatments arranged in k = 3 rows and s = 4 columns in each of r = 2 replications is used to demonstrate the output from the RRC module. The steps to construct this design are:

1. Click on the Gendex icon on the DESKTOP and then on BIB.BAT to use the BIB module to construct a resolvable incomplete block design. The ALPHA or CIB module could have been selected. Alternatively, go to START/PROGRAMS/MS_DOS PROMPT and change directory to C:\Gendex>. Type in BIB (or type in java -cp C:\Gendex Bib).
2. Answer the following options when prompted:
   Choose the number of treatments? 12 was selected.
   Choose the block size? 3 was selected.
   Choose the number of replications? 2 was selected.
   Do you want a 1-resolvable design? YES was selected.
   Enter a random seed? Cancel was selected.
   Enter number of tries? Cancel was selected.
3. When the incomplete block experiment design appears on the screen, click OK at the bottom of the screen. The next screen gives a description of the plan just constructed with the note "Note: BIB.HTM has been created."
4. Open WINDOWS EXPLORER, click on C:\ and then on Gendex. Highlight BIB.HTM. Under FILE, click on OPEN
5. From EDIT, click on SELECT ALL and then on COPY.
6. Return to DOS and type "C:\Gendex>notepad abc.txt" where abc.txt is the name of the input file for RRC . Answer YES to create a new file.
7. From EDIT, click on PASTE and the unedited version of BIB.HTM appears.
8. Edit out all material except the randomized plan. Remove all blank lines and select SAVE.
9. In DOS use the command "C:\Gendex>RRC" and return.
10. Click on abc.txt from the menu that appears. Select OPEN and answer YES for queries on r replications, k rows, and s columns. Click OK to the remaining queries.
11. When the randomized form of the randomized plan appears on the screen, click OK at the bottom of the screen. A screen will appear describing the design just created with the note "Note: RRC.HTM has been created."
12. To print RRC.HTM, return to WINDOWS EXPLORER. Click on the Gendex folder and highlight the RRC.HTM file. From FILE, select PRINT.

The output obtained was:

RRC 2.1: Construct a resolvable row-column design of size (r,k,s)
(C) 2001 Design Computing (URL: http://designcomputing.hypermart.net)

Note: Resolvable row-column design for v=12, r=2, k=3 and s=4.

| | |
|---|---|
| try # | 1 |
| seed | 999539883190 |
| # of iterations | 2 |
| f | 92.0000 |
| E(column) | 0.5946 |
| E(row) | 0.6735 |
| E | 0.4146 |
| E/U | 0.8681 |

| | |
|---|---|
| try # | 2 |
| seed | -1028198081 |
| # of iterations | 6 |
| f | 86.6667 |
| E(column) | 0.5946 |
| E(row) | 0.6735 |
| E | 0.4615 |
| E/U | 0.9664 |

| | | | |
|---|---|---|---|
| 1 | 4 | 7 | 11 |
| 0 | 5 | 6 | 9 |
| 2 | 3 | 8 | 10 |

| | | | |
|---|---|---|---|
| 5 | 11 | 8 | 0 |
| 7 | 3 | 1 | 10 |
| 2 | 6 | 9 | 4 |

Note: RRC used 0.11 seconds.
Note: this software is licensed to AV Biometrics (Australia).

To obtain an edited copy of RRC.HTM, the output needs to be copied and pasted into a word processing program. The resolvable 3-row by 4 column experiment design was obtained in 0.11 seconds of computer time. Two tries were used and an E/U ratio of 0.9664 resulted. Perhaps another attempt would result in a higher E/U ratio but this may be the best that can be achieved.

As a second example, let v = 16 treatments in k = 4 rows and s = 4 columns in r = 5 complete blocks. The resulting design should be a balanced lattice square experiment design. Following the above steps, the output obtained was:

BIB 2.1: Construct incomplete block designs of size (v,k,r)
(C) 2001 Design Computing (URL: http://designcomputing.hypermart.net/gendex)

Note: Incomplete block design for v=16, k=4, r=5, b=20.

| | |
|---|---|
| try # | 1 |
| seed | 1002378225680 |
| # of iterations | 13 |
| E | 0.7891202 |
| E/U | 0.9864 |
| concurrences | 0(13) 1(94) 2(13) |

| | |
|---|---|
| try # | 2 |

| | |
|---|---|
| seed | -1660937685 |
| # of iterations | 16 |
| E | 0.79328436 |
| E/U | 0.9916 |
| concurrences | 0(8) 1(104) 2(8) |

| | |
|---|---|
| try # | 8 |
| seed | -1332855961 |
| # of iterations | 11 |
| E | 0.8 |
| E/U | 1.0000 |
| concurrences | 1(120) |

Plan (Blocks are columns):

| | | | |
|---|---|---|---|
| 10 | 8 | 0 | 14 |
| 1 | 5 | 15 | 9 |
| 4 | 2 | 6 | 7 |
| 13 | 11 | 3 | 12 |

| | | | |
|---|---|---|---|
| 11 | 4 | 14 | 0 |
| 12 | 8 | 6 | 7 |
| 3 | 9 | 13 | 2 |
| 1 | 15 | 5 | 10 |

| | | | |
|---|---|---|---|
| 6 | 4 | 0 | 7 |
| 10 | 3 | 13 | 1 |
| 8 | 14 | 9 | 5 |
| 12 | 2 | 11 | 15 |

| | | | |
|---|---|---|---|
| 4 | 8 | 10 | 1 |
| 12 | 13 | 15 | 2 |
| 0 | 7 | 14 | 9 |
| 5 | 3 | 11 | 6 |

| | | | |
|---|---|---|---|
| 12 | 4 | 14 | 9 |
| 15 | 6 | 0 | 3 |
| 13 | 7 | 8 | 10 |
| 2 | 11 | 1 | 5 |

Note: BIB used 0.22 seconds.
Note: this software is licensed to AV Biometrics.

This is a randomized form of a balanced lattice square experiment design. This is indicated by the efficiency factors for rows and for columns, each one being 0.8. Each treatment geometric component is confounded with rows in one of the complete blocks and is unconfounded in the other four complete blocks. Hence, the intra-block efficiency factor is 4/5 = 0.8. The same holds for columns. The E/U ratio is one as it should be.

## COMMENTS

This toolkit offers the experimenter a very high degree of flexibility in choosing a plan that fits the conditions of the experiment. This allows one to *design for the*

*experiment and not to experiment for the design* since many, many types of designs do not appear in any catalogue of designs. One such example was presented above for v = 25 treatments with r = 4 replicates arranged in a 10 × 10 square. Optimal or near optimal plans are obtained in all cases. Only a relatively short amount of computer time is used to obtain plans, even those for very large numbers of treatments and replicates. Obtaining a randomized plan for v = 10,000 treatments in incomplete blocks of size k = 5 with r = 6 replications would require a very large amount of time if done manually, several days at least. Note that such a plan would not appear in any catalogue and would need to be constructed prior to randomization. Although a simple method of construction for such a design exists (See Federer, 1993, Section 10.4.2), it still would require a large amount of time. Also, a printed form of the randomized plan is easily obtained. The time saving properties of this tool kit cannot be over emphasized. Such a toolkit will considerably increase the efficiency of experimenters' programs and allow considerable flexibility in the selection of an experiment design. The experimenter may not know exactly what plan can be used at an experimental site until it is time to lay-out the experiment. On such occasions, several possible plans may easily be printed allowing the experimenter to use the one that fits the situation.

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